

10047253.011402

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AMSH1 -----MFDHIDVSLSPFEERVRLSKLGCNITISEDITPRR 35
AMSH2 MDQPTTVNLSKKLAAMPDHTDVSLSFEERVRLSKLGCNITISEDITPRR 50
AMSH -----MSDHGDVSLFPEDRVRLSQLGSAVEVNEDIFPRR 35
          *** ***,**,* ***,**,* ***,**,* ***,**,* ***,**,*
AMSH1 YERSGVEMERMASVYLEEGNLENAFVLYNKFTITLFVEKLENHRDYMQQCAV 85
AMSH2 YFRSGVEMERMASVYLEEGNLENAFVLYNKFTITLFVEKLENHRDYMQQCAV 100
AMSH YFRSGVEIIRMASYSEE GNIEHAFLYLYNKFTITLFIEKLEKHRDYKSAVI 85
          ***** ***,**,* ***,**,* ***,**,* ***,**,* ***,**,* ***,**,*
AMSH1 PEKQDIMKKLKEIAFFRTDELENDLLKYNVEYQEYLQSKNKYKAEILKK 135
AMSH2 PEKQDIMKKLKEIAFFRTDELENDLLKYNVEYQEYLQSKNKYKAEILKK 150
AMSH PEKQDITVKKLKEIAFFKAEIKAEILKKYTKKEYTEYNEKKKAEELARN 135
          ***,* ***,**,* ***,**,* ***,**,* ***,**,* ***,**,* ***,**,*
AMSH1 LEHQRLIEAERKRIAQMROQQLESEQTLFFEDQLKKQELARGQMRSQQTS 185
AMSH2 LEHQRLIEAERKRIAQMROQQLESEQTLFFEDQLKKQELARGQMRSQQTS 200
AMSH MAIQQELIEKEKQVVAQKQKQQLQEQTHATEEMIRNQLERKRLKIVQEF 185
          * **,* **,* **,* **,* **,* **,* **,* **,* **,* **,*
AMSH1 G-LSAQIDGSALSCHS--THQNNSLNVFADQPNKSDATNYASHSPFVNR 232
AMSH2 G-LSAQIDGSALSCHS--THQNNSLNVFADQPNKSDATNYASHSPFVNR 247
AMSH GKVDPGIGGGLVPLEKPSLDVFPTLTVSSIQPSDCHTVRPAKPFVVD 235
          * **,* **,* **,* **,* **,* **,* **,* **,* **,* **,*
AMSH1 ALTPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNTVRGIETCGIL 282
AMSH2 ALTPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNTVRGIETCGIL 297
AMSH SLKPGALSNESEIPTIDGLRHVVVGRRLCPQLQLASANTARGVETCGIL 285
          **,* **,* **,* **,* **,* **,* **,* **,* **,* **,*
AMSH1 CGKLTNEFTTIHVIVPKQSAGPDYCDMENVEELENVQDQHDLLTLGWI 332
AMSH2 CGKLTNEFTTIHVIVPKQSAGPDYCDMENVEELENVQDQHDLLTLGWI 347
AMSH CGKLMRNEFTTIHVIVPKQSAGSDYCNTEKEELNLIQDQDGLTLGWI 335
          **** ***,**,* ***,**,* ***,**,* ***,**,* ***,**,* ***,**,*
AMSH1 TPTQTAFLLSSVLETHC SYQLMLPEAI AIVCS EKHRDTGIFRLNAGML 382
AMSH2 TPTQTAFLLSSVLETHC SYQLMLPEAI AIVCS EKHRDTGIFRLNAGML 397
AMSH TPTQTAFLLSSVLETHC SYQLMLPEAI AIVCS EKHRDTGIFRLNAGML 385
          ***** ***,**,* ***,**,* ***,**,* ***,**,* ***,**,* ***,**,*
AMSH1 EVSACKKKGFHPHTKEPRLFISICKHV--LVKDIXIIVLDLR----- 421
AMSH2 EVSACKKKGFHPHTKEPRLFISICKHV--LVKDIXIIVLDLR----- 447
AMSH EISCRQKGFHPHTKEPRLFISICKHV--LVKDIXIIVLDLR----- 424
          **,* **,* **,* **,* **,* **,* **,* **,* **,* **,*
AMSH1 -----
AMSH2 LLGISRSSSPSEQL 461
AMSH -----

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FIGURE 2

COP9_su5_Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm	VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At	AGRLENVVVGWYHSHPGYGCWLSGIDVSTQRLNQHQEPFLA--VVIDPTRTVSAGKVEIG
COP9_su5_Ce	EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
AF2198_Arcfu	LPIGMKVFGTVHSHSPSPCRPSEEDLSLFTRFGKYHIIVCY--PYDENSWKCYNRKGEEV
PH0451_Pyrho	MPHDESIKGTTFHSHSPFPYPSEGDLMFFSKFGGIHIIAAF--PYDEDSVKAFDSEGREV
TVN1035_Thevo	KPIDFSLVGSVHSHPSGITKPSDEDLRMFSLTGKIHIIVGY--PYNLKDYSAYDRSGNKV
MTH971_Metth	LPPFTGAVGSVHSHPGPVNLPAAADLHFFSKNGLFHIIAH--PYTMETVAAYTRNGDPV
aq_1691_Aquae	ISKGMEIVGVYHSHPDHPDRPSQFDLQRAFPDLSYIIFSVQ--KGKVASYRSWELKGDKF
RV1334_Myctu	EDADEVPVVIYHSHTATEAYPSRTDVKLATEPDAHYVLVSTRDPHRHELRSYRIVDGAVT
RadC_Ecoli	IKINASALILAHNHPSGCAEPSKADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA
.....HSHP.....S'D

FIGURE 3

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COP9_bu5_Hs	VGRLNAIGWYHSHPGYGCWLSGIDVSTQMLNQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm	VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At	AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQHQEPFLA--VVIDPTRTVSAGKVEIG
COP9_su5_Ce	EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
Pad1_Dm	TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Pad1_Hs	TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Sks1_Pd	TGRDEIVIGWYHSHPGFGCWLSVDVNTQQSFEQLQSRVA--VVVDPLQSVRG-KVVID
Pad1_Sc	TGRDOMVVGWYHSHPGFGCWLSVDVNTQKSFEQLNSRAVA--VVVDPIQSVKG-KVVID
.....	HSHP''''''S 'D

FIGURE 4

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